Resource Summary Report

Generated by dkNET on Apr 17, 2025

DISENTANGLER

RRID:SCR_009161
Type: Tool

Proper Citation

DISENTANGLER (RRID:SCR_009161)

Resource Information

URL: http://kumasakanatsuhiko.jp/projects/disentangler/

Proper Citation: DISENTANGLER (RRID:SCR_009161)

Description: Software application that is a visualization technique for linkage disequilibrium mapping and haplotype analysis of multiple multi-allelic genetic markers. (entry from Genetic Analysis Software)

Abbreviations: DISENTANGLER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, java/jre1.5, bio.tools

Funding:

Resource Name: DISENTANGLER

Resource ID: SCR_009161

Alternate IDs: nlx_154284, bIotools:disentangler

Alternate URLs: https://bio.tools/disentangler

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063538+0000

Ratings and Alerts

No rating or validation information has been found for DISENTANGLER.

No alerts have been found for DISENTANGLER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Liu Z, et al. (2024) Human leukocyte antigen-DQA1*04:01 and rs2040406 variants are associated with elevated risk of childhood Burkitt lymphoma. Communications biology, 7(1), 41.

Valenzuela-Ponce H, et al. (2023) Honduras HIV cohort: HLA class I and CCR5-?32 profiles and their associations with HIV disease outcome. Microbiology spectrum, 11(6), e0161323.

Dallmann-Sauer M, et al. (2020) The complex pattern of genetic associations of leprosy with HLA class I and class II alleles can be reduced to four amino acid positions. PLoS pathogens, 16(8), e1008818.

Ferreiro-Iglesias A, et al. (2018) Fine mapping of MHC region in lung cancer highlights independent susceptibility loci by ethnicity. Nature communications, 9(1), 3927.